

10 30 50
 TTCGGGCACGAGGGCAGGATGGCGCCACCACCAGCTAGAGTACATCTAGGTGCGTTCCTG
 M A P P P A R V H L G A F L
 70 90 110
 GCAGTGACTCCGAATCCCGGGAGCGCAGCGAGTGGGACAGAGGCAGCCGCGGCCACACCC
 A V T P N R G S A A S G T E A A A A T P
 130 150 170
 AGCAAAGTGTGGGGCTCTTCCGCGGGGAGGATTGAACCACGAGGCGGGGGCCGAGGAGCG
 S K V W G S S A G R I E P R G G G R G A
 190 210 230
 CTCCCTACCTCCATGGGACAGCACGGACCCAGTGCCCGGGCCCGGGCAGGGCGCGCCCCA
 L P T S M G Q H G P S A R A R A G R A P
 250 270 290
 GGACCCAGGCGCGCGGAAGCCAGCCCTCGGCTCCGGGTCCACAAGACCTTCAAGTTT
 G P R P A R E A S P R L R V H K T F K F
 310 330 350
 GTCGTCGTCGGGGTCTGCTGCAGGTCGTACCTAGCTCAGCTGCAACCATCAAACCTTCAT
 V V V G V L L Q V V P S S A A T I K L H
 370 390 410
 GATCAATCAATTGGCACACAGCAATGGGAACATAGCCCTTTGGGAGAGTTGTGTCCACCA
 D Q S I G T Q Q W E H S P L G E L C P P
 430 450 470
 GGATCTCATAGATCAGAACGTCCTGGAGCCTGTAACCGGTGCACAGAGGGTGTGGGTTAC
 G S H R S E R P G A C N R C T E G V G Y
 490 510 530
 ACCAATGCTTCCAACAATTTGTTTGCTTGCCTCCCATGTACAGCTTGTAAATCAGATGAA
 T N A S N N L F A C L P C T A C K S D E
 550 570 590
 GAAGAGAGAAGTCCCTGCACCACGACCAGGAACACAGCATGTCAGTGCAAACCAGGAAC
 E E R S P C T T T R N T A C Q C K P G T
 610 630 650
 TTCCGGAATGACAATTCTGCTGAGATGTGCCGGAAGTGCAGCACAGGGTGCCCCAGAGGG
 F R N D N S A E M C R K C S T G C P R G
 670 690 710
 ATGGTCAAGGTCAAGGATTGTACGCCCTGGAGTGACATCGAGTGTGTCCACAAAGAATCA
 M V K V K D C T P W S D I E C V H K E S

FIG.1A

730 750 770
 GGCAATGGACATAATATATGGGTGATTTTGGTTGTGACTTTGGTTGTTCCGTTGCTGTTG
 G N G H N I W V I L V V T L V V P L L L

 790 810 830
 GTGGCTGTGCTGATTGTCTGTTGTCATCGGCTCAGGTTGTGGAGGGGACCCCAAGTGC
 V A V L I V C C C I G S G C G G D P K C

 850 870 890
 ATGGACAGGGTGTGTTTCTGGCGCTTGGGTCTCCTACGAGGGCCTGGGGCTGAGGACAAT
 M D R V C F W R L G L L R G P G A E D N
 910 930 950
 GCTCACAACGAGATTCTGAGCAACGCAGACTCGCTGTCCACTTTCTGTCTCTGAGCAGCAA
 A H N E I L S N A D S L S T F V S E Q Q
 970 990 1010
 ATGGAAAGCCAGGAGCCGGCAGATTTGACAGGTGTCACTGTACAGTCCCCAGGGGAGGCA
 M E S Q E P A E L T G V T V Q S P G E A
 1030 1050 1070
 CAGTGTCTGCTGGGACCGGCAGAAGCTGAAGGGTCTCAGAGGAGGAGGCTGCTGGTTCCA
 Q C L L G P A E A E G S Q R R R L L V P
 1090 1110 1130
 GCAAATGGTGCTGACCCCACTGAGACTCTGATGCTGTTCTTTGACAAGTTTGCAAACATC
 A N G A D P T E T L M L F F D K F A N I
 1150 1170 1190
 GTGCCCTTTGACTCCTGGGACCAGCTCATGAGGCAGCTGGACCTCACGAAAAATGAGATC
 V P F D S W D Q L M R Q L D L T K N E I
 1210 1230 1250
 GATGTGGTCAGAGCTGGTACAGCAGGCCAGGGGATGCCTTGTATGCAATGCTGATGAAA
 D V K R A G T A G P G D A L Y A M L M K
 1270 1290 1310
 TGGGTCAACAAAACCTGGACGGAACGCCTCGATCCACACCCTGCTGGATGCCTTGGAGAGG
 W V N K T G R N A S I H T L L D A L E R
 1330 1350 1370
 ATGGAAGAGAGACATGCAAAAGAGAAGATTCAGGACCTCTTGGTGGACTCTGGAAAGTTC
 M E E R H A K E K I Q D L L V D S G K F

FIG.1B

1390	1410	1430
ATCTACTTAGAAGATGGCACAGGCTCTGCCGTGTCCTTGGAGTGAAAGACTCTTTTACC		
I Y L E D G T G S A V S L E		
1450	1470	1490
AGAGGTTTCCTCTTAGGTGTTAGGAGTTAATACATATTAGGTTTTTTTTTTTAAACAT		
1510	1530	1550
GTATACAAAGTAAATTCTTAGCCACGTGTATTGGCTCCTGCCTGTAATCCCATCACTTTG		
1570	1590	1610
GGAGGCTGACGCCGGTGGATCCACTTGAGGTCCGAAGTTCCAAGACCAGCCCTGAACCAA		
1630	1650	1670
CATCGTGGAAATGCCCGTCTTTTACAAAAAATACCAAAAATTCAACTGGAATGTGCATG		
1690	1710	1730
GTGTGTGCCATCATTTCTCGGCTAACTACGGGAGGTCTGAGGCCAGGAGAATCCACTTG		
1750	1770	1790
AACCCACGAAGGACAGTGTAGACTGCAGATTGCACCACTGCACTCCCAGCCTGGGAACA		
1810	1830	1850
CAGAGCAAGACTCTGTCTCAAGATAAAATAAAATAAACTTGAAAGAATTATTGCCCGACT		
1870	1890	1910
GAGGCTCACATGCCAAAGGAAAATCTGGTTCTCCCCTGAGCTGGCCTCCGTGTGTTTCCT		
1930	1950	1970
TATCATGGTGGTCAATTGGAGGTGTTAATTTGAATGGATTAAGGAACACCTAGAACACTG		
1990	2010	2030
GTAAGGCATTATTTCTGGGACATTATTTCTGGGCATGTCTTCGAGGGTGTTCAGAGGG		
2050	2070	2090
GATTGGCATGCGATCGGGTGGACTGAGTGAAAAAGACCTACCCCTTAATTTGGGGGGGCAC		
2110	2130	2150
CGTCCGACAGACTGGGGAGCAAGATAGAAGAAAAACAAAAAAAAAAAAAAAAAAAA		

FIG.1C

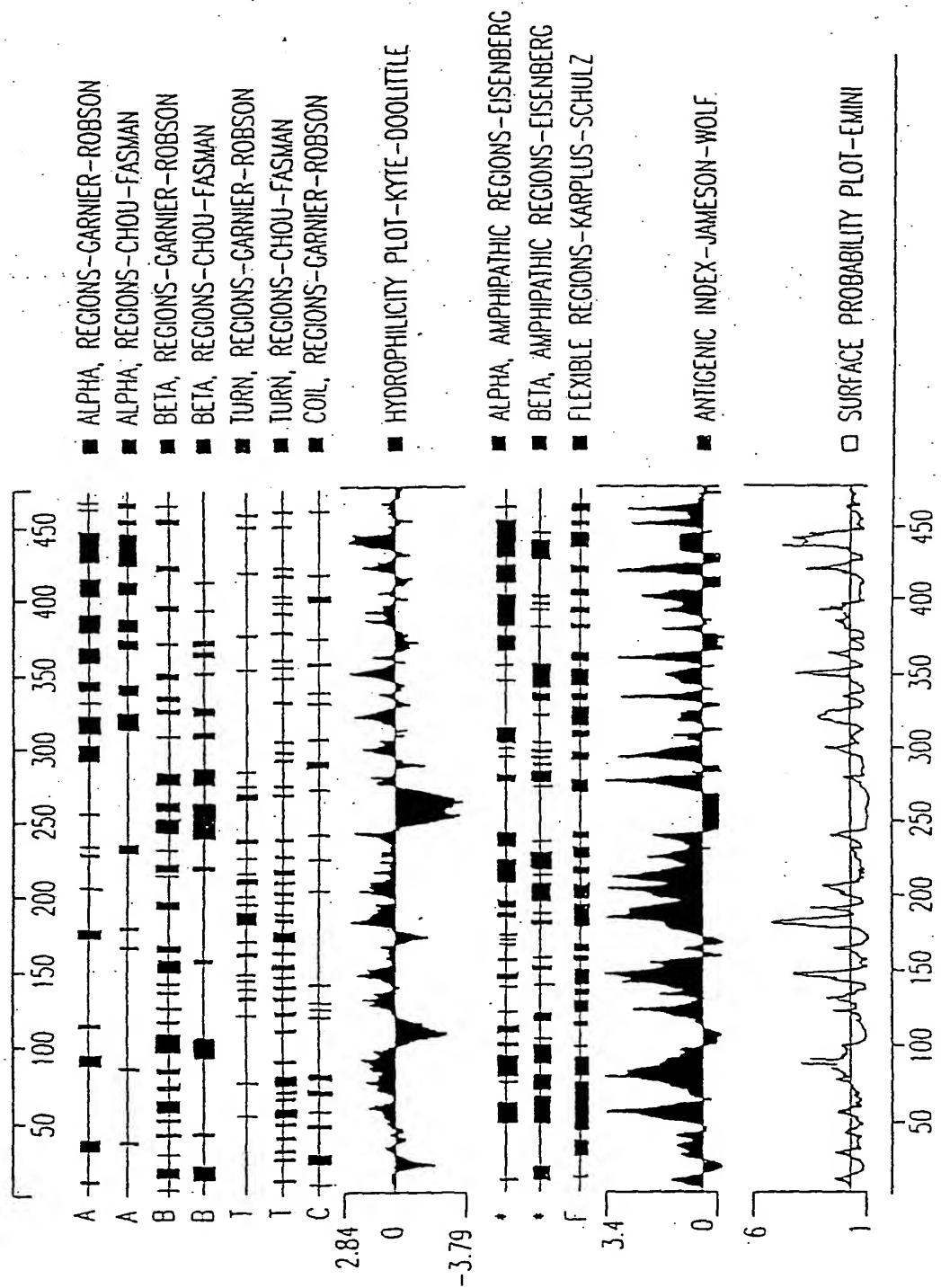


FIG.3

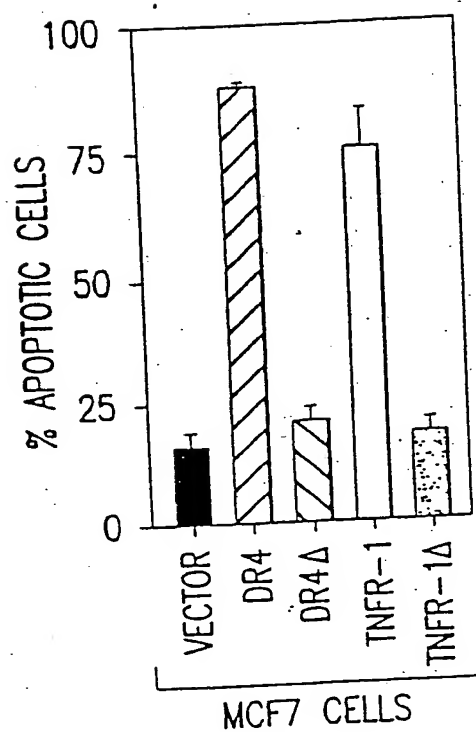
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51 TCAATTGGCA CACAGCAATG GGAAACATAG CCCTTTGGAA GANTTGTNTC
101 CACCAGGATC TCATAGATCA AAACATCCTG GGAGCCTGTT AACCGGTGCC
151 CCAAAGGNTG GTCAAGGTCA AGGAATTGTT NCGCCCTGGA AGTGAACATC
201 GAGTGTNTCC ACAAAGGATT CAGGCAATGG GACATAAATA TATGGGTGAA
251 TTTTGGTTGT GAACTTTGGT TGNTCCCGTT GNTGTTGNTG GCTGTGCTGA
301 TTGTTTGTG TTGCATCGGC TTCAGGTTNT GGAGGGGGAC CCAAGTGCAT
351 GGACAGGGTG TGTTTCTGGG GTTTGGGTCT CTTAGAGGGC NTGGGTTANG
401 GCANGTTCAC AAGGGTTTTA GCAANG
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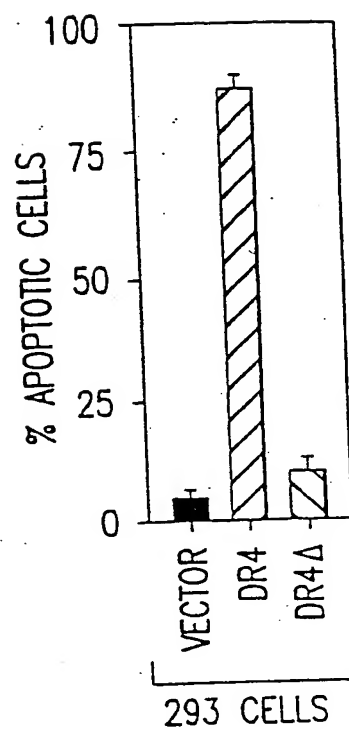
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1  TGGGGCTGAG GACAATGCTG ACNACGAGAT TCTGAGCAAC GCAGNACTNG
51 CTGTCCACTT TCGTCTNTGN GCAGCAAATG GAAAGCCAGG AGCCGGCAGA
101 TTTGACAGGT GTCAGTGTAC AGTCCCCAGG GGAGGCACAG TGTCTGCTGG
151 TGAGTTGGGG ACAGGCCCTT GCAAGACCTT GTGAGGCAGG GGGTGAAGGC
201 CATGNCTCGG CTTNNNTGG TCAAAGGGGA AGTGGAGCCT GAGGGAGATG
251 GGACTIONAGG GGGACGGNGC TGCGTGGGGA AAAAGCAGCC ACCNTTTGAC
301 AAGGGGGACA GGCATTTTTN CAAATGTGTG CTTNTTGGT
```

FIG.4



MCF7 CELLS
FIG.5A



293 CELLS
FIG.5B

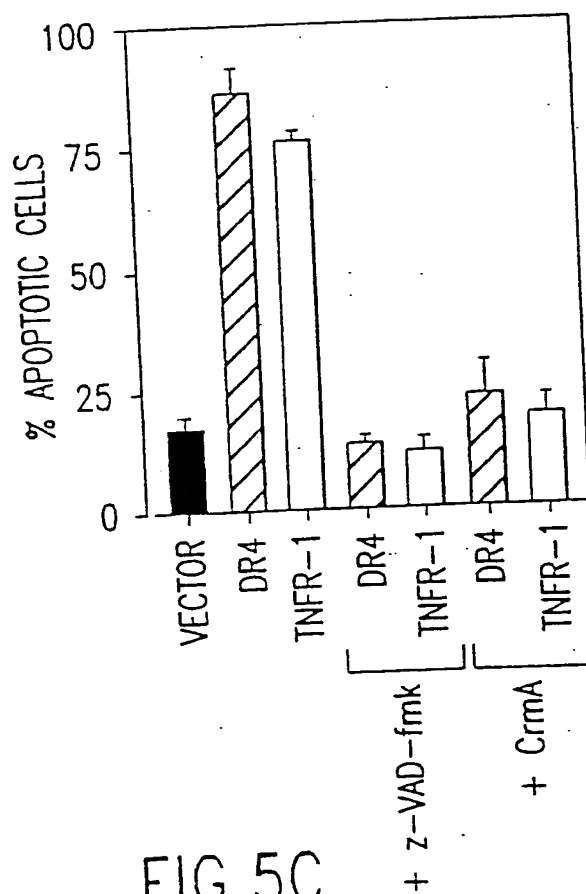


FIG.5C

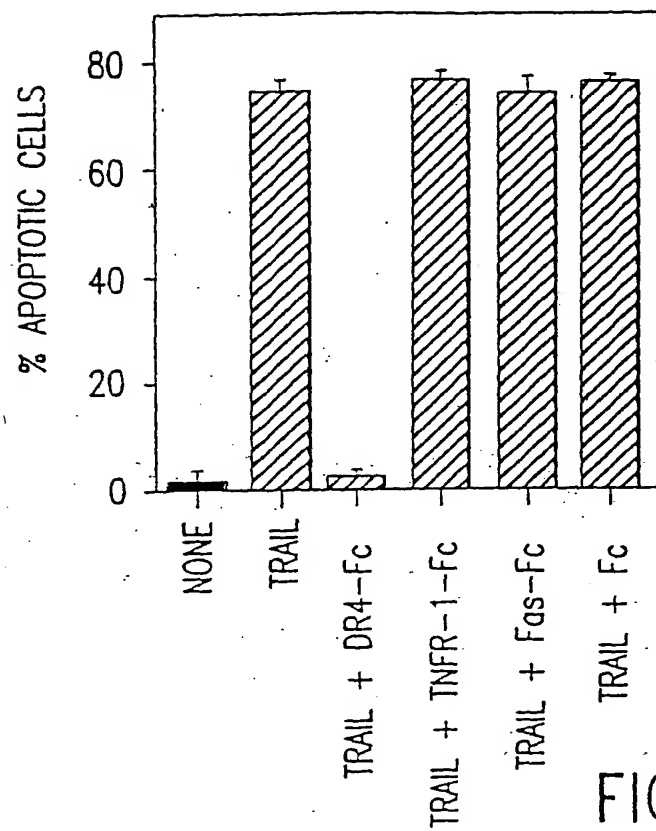


FIG.6A

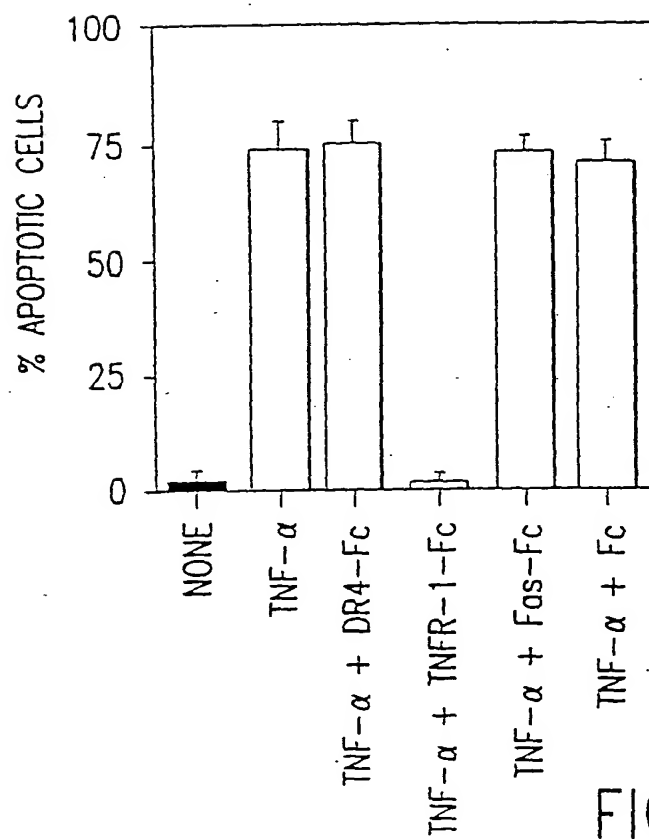


FIG.6B